

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 05:40:06 ; Search time 1838.32 Seconds
(without alignments)
12203.124 Million cell updates/sec

Title: US-09-811-118-2

Perfect score: 1072
Sequence: 1 GAGCCGCGCACCTCCGAGAC.....TTGCATCCACATGATTTTC 1072

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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1	1072	100.0	1072	6	AR151077	AR151077 Sequence
2	921	85.9	1511	6	AX188360	AX188360 Sequence
3	919	85.7	1228	9	AK027683	AK027683 Homo sapi
4	916	85.4	1227	6	AX080813	AX080813 Sequence
5	667	62.2	857	9	AF091092	AF091092 Homo sapi
6	629	58.7	1251	6	AX080809	AX080809 Sequence
7	596	55.6	160066	2	AL356976	AL356976 Homo sapi
8	361	33.7	751	6	AX186595	AX186595 Sequence
9	356	33.2	468	6	AX187668	AX187668 Sequence
10	151	14.1	51381	2	AF322456	AF322456 Homo sapi
11	80	7.5	51381	2	AF322456	AF322456 Homo sapi
12	79	7.4	55891	2	AC022847	AC022847 Homo sapi
13	50	4.7	50	6	AX080812	AX080812 Sequence
14	49	4.6	1033	10	BC003228	BC003228 Mus muscu
15	46	4.3	241048	2	AL627238	AL627238 Mus muscu
16	44	4.1	164683	2	AC097883	AC097883 Rattus no
17	27	2.5	100000	9	AP000077	AP000077 Homo sapi
18	27	2.5	100414	9	AC001056	AC001056 Homo sapi
19	27	2.5	158523	2	AC013547	AC013547 Homo sapi
20	27	2.5	166009	2	AC011061	AC011061 Homo sapi
21	26	2.4	164683	2	AC097883	AC097883 Rattus no
22	25	2.3	129090	2	AC083951	AC083951 Homo sapi
23	25	2.3	182947	2	AC046176	AC046176 Homo sapi
24	25	2.3	201408	9	AC090644	AC090644 Homo sapi
25	24	2.2	24	6	AX080810	AX080810 Sequence
26	24	2.2	24	6	AX080811	AX080811 Sequence
27	24	2.2	140781	2	AC008611	AC008611 Homo sapi
28	24	2.2	141513	9	AC020905	AC020905 Homo sapi
29	24	2.2	164468	2	AC021899	AC021899 Homo sapi
30	24	2.2	165201	2	AC090597	AC090597 Homo sapi
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33	24	2.2	193424	4	AC005690	AC005690 Homo sapi
34	24	2.2	197836	4	AC090032	AC090032 Canis fam
35	24	2.2	197901	2	AC018621	AC018621 Homo sapi
36	24	2.2	200204	9	AC018626	AC018626 Homo sapi
37	24	2.2	205416	2	AC107388	AC107388 Homo sapi
38	24	2.2	207677	2	AP001497	AP001497 Homo sapi
39	23	2.1	767	10	AF045769	AF045769 Mus muscu
40	23	2.1	876	10	AF045768	AF045768 Mus muscu
41	23	2.1	958	10	D87896	D87896 Mus muscu
42	23	2.1	989	10	AF274027	AF274027 Mus muscu
43	23	2.1	1380	10	AF044056	AF044056 Mus muscu
44	23	2.1	2075	10	MM0291744	MM0291744 Mus muscu
45	23	2.1	3980	10	MM0212104	MM0212104 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS AR151077 AR151077 1072 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6231853.
ACCESSION AR151077
VERSION AR151077.1 GI:15117127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1072)
AUTHORS Hillman,J.L., Corley,N.C. and Patterson,C.
TITLE Human glutathione peroxidase-6
JOURNAL Patent: US 6231853-A 2 15-MAY-2001;
FEATURES
source location/Qualifiers
1..1072
/organism="unknown"
BASE COUNT 275 a 294 c 270 g 233 t
ORIGIN

Query Match 100.0%; Score 1072; DB 6; Length 1072;
Best local Similarity 100.0%; Pred. No. 0;

Matches 1072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GAGCCGCCACCTCCGGAACAGCAGATGTCGGCGACGGTGGCAGCGCGTGTCT	60						
Db	1	GAGCCGCCACCTCCGGAACAGCAGATGTCGGCGACGGTGGCAGCGCGTGTCT	60						
QY	61	CTGTGGGCTGCGGCTGCGCGACAGCAGAGCAGAGCTTCTACGACTTCAAGCGGTCAA	120						
Db	61	CTGTGGGCTGCGGCTGCGCGACAGCAGAGCAGAGCTTCTACGACTTCAAGCGGTCAA	120						
QY	121	CATCCGGGGCAAACTGGTGTGCTGGAGAGTACCGGGATCGGTGTCCCGGGTGGAA	180						
Db	121	CATCCGGGGCAAACTGGTGTGCTGGAGAGTACCGGGATCGGTGTCCCGGGTGGAA	180						
QY	181	TGTGGCCAGCAGTGCAGCTTACAGACAGCAGCTACGAGCCCTGACAGCAGTGCAGCG	240						
Db	181	TGTGGCCAGCAGTGCAGCTTACAGACAGCAGCTACGAGCCCTGACAGCAGTGCAGCG	240						
QY	241	AGACCTGGGCCCCCACCACCTTCAACGTGTCTGCTTCCCTGCAACGATTGGCCAA	300						
Db	241	AGACCTGGGCCCCCACCACCTTCAACGTGTCTGCTTCCCTGCAACGATTGGCCAA	300						
QY	301	GAGCCCTGACAGCAACAGAGATTGAGAGCTTGCCTGCCGACCTACAGTGTCTAT	360						
Db	301	GAGCCCTGACAGCAACAGAGATTGAGAGCTTGCCTGCCGACCTACAGTGTCTAT	360						
QY	361	CCCATGTTTACAGAGATTGCACTACCGGTACTGTGTCCTGCTGCTTCAAGTACT	420						
Db	361	CCCATGTTTACAGAGATTGCACTACCGGTACTGTGTCCTGCTGCTTCAAGTACT	420						
QY	421	GGCCCAACTTTCGGGAAAGAGCCCACTGTAAGTGTGGAAGTACTAGTACGCCCA	480						
Db	421	GGCCCAACTTTCGGGAAAGAGCCCACTGTAAGTGTGGAAGTACTAGTACGCCCA	480						
QY	481	TGGAAGGTGTGGAGGCTTGGGACCCCACTGTCTAGTGGAGAGGTGCAGCTCAGAT	540						
Db	481	TGGAAGGTGTGGAGGCTTGGGACCCCACTGTCTAGTGGAGAGGTGCAGCTCAGAT	540						
QY	541	CACAGCGCTGTGAGAGAGCTCCTACTGTAAGCGAAGACTTATPACCACCGGCTCT	600						
Db	541	CACAGCGCTGTGAGAGAGCTCCTACTGTAAGCGAAGACTTATPACCACCGGCTCT	600						
QY	601	CTCTCTCACACCTTATCCCGCCACCTGTGTGGGCTACCAATCCAAATCAATAG	660						
Db	601	CTCTCTCACACCTTATCCCGCCACCTGTGTGGGCTACCAATCCAAATCAATAG	660						
QY	661	TGCTTAAAGGAGAGACCACTGACTCTCTCTTACTTACTTATGCAATTTGGTCCAT	720						
Db	661	TGCTTAAAGGAGAGACCACTGACTCTCTCTTACTTACTTATGCAATTTGGTCCAT	720						
QY	721	CATTCTTGTGGGGAAAAATTTCTAGTATTTTGTATTTTGAATCTTACAGCAACAAATAG	780						
Db	721	CATTCTTGTGGGGAAAAATTTCTAGTATTTTGTATTTTGAATCTTACAGCAACAAATAG	780						
QY	781	GAACTCTGGCCATGAGAGCTTGTGACAGTGAATCACCAGCCGATACGAGCTCTTGC	840						
Db	781	GAACTCTGGCCATGAGAGCTTGTGACAGTGAATCACCAGCCGATACGAGCTCTTGC	840						
QY	841	CAACAAAAATGTGTGCAATATAGATATCAAGCAATATCTCCACCCAAAGGCTTCT	900						
Db	841	CAACAAAAATGTGTGCAATATAGATATCAAGCAATATCTCCACCCAAAGGCTTCT	900						
QY	901	GTAAGCTGGAGCAATGATTACCTCATAGGGCTTGTGTGAGGATTAGATGAATACCTG	960						
Db	901	GTAAGCTGGAGCAATGATTACCTCATAGGGCTTGTGTGAGGATTAGATGAATACCTG	960						
QY	961	TGAAAGTGTCTAGGAGTGCAGCAATATAGAGGCAATTAATGACATTTTTCATAT	1020						
Db	961	TGAAAGTGTCTAGGAGTGCAGCAATATAGAGGCAATTAATGACATTTTTCATAT	1020						
QY	1021	AAACCAAAAAATATCTTGTATCAATAAAAACTTGCATCAACATGAATTC	1072						
Db	1021	AAACCAAAAAATATCTTGTATCAATAAAAACTTGCATCAACATGAATTC	1072						

Query Match									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1021; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1	GAGCCGCCACCTCCGGAACAGCAGATGTCGGCGACGGTGGCAGCGCGTGTCT	60						
Db	276	GAGCCGCCACCTCCGGAACAGCAGATGTCGGCGACGGTGGCAGCGCGTGTCT	335						
QY	61	CTGTGGGCTGCGGCTGCGCGACAGCAGAGCAGAGCTTCTACGACTTCAAGCGGTCAA	120						
Db	336	CTGTGGGCTGCGGCTGCGCGACAGCAGAGCAGAGCTTCTACGACTTCAAGCGGTCAA	395						
QY	121	CATCCGGGGCAAACTGGTGTGCTGGAGAGTACCGGGATCGGTGTCCCGGGTGGAA	180						
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QY	181	TGTGGCCAGCAGTGCAGCTTACAGACAGCAGCTACGAGCCCTGACAGCAGTGCAGCG	240						
Db	456	TGTGGCCAGCAGTGCAGCTTACAGACAGCAGCTACGAGCCCTGACAGCAGTGCAGCG	515						
QY	241	AGACCTGGGCCCCCACCACCTTCAACGTGTCTGCTTCCCTGCAACGATTGGCCAA	300						
Db	516	AGACCTGGGCCCCCACCACCTTCAACGTGTCTGCTTCCCTGCAACGATTGGCCAA	575						
QY	301	GGAAGCTGTGAGAGAGATTGAGAGCTTGCCTGCGCACTTACAGTGTCTAT	360						
Db	576	GGAAGCTGTGAGAGAGATTGAGAGCTTGCCTGCGCACTTACAGTGTCTAT	635						
QY	361	CCCATGTTTACAGAGATTGCACTACCGGTACTGTGTCCTGCTGCTTCAAGTACT	420						
Db	636	CCCATGTTTACAGAGATTGCACTACCGGTACTGTGTCCTGCTGCTTCAAGTACT	695						
QY	421	GGCCCAACTTTCGGGAAAGAGCCCACTGTAAGTGTGGAAGTACTAGTACGCCCA	480						
Db	696	GGCCCAACTTTCGGGAAAGAGCCCACTGTAAGTGTGGAAGTACTAGTACGCCCA	755						
QY	481	TGGAAGGTGTGGAGGCTTGGGACCCCACTGTCTAGTGGAGAGGTGCAGCTCAGAT	540						
Db	756	TGGAAGGTGTGGAGGCTTGGGACCCCACTGTCTAGTGGAGAGGTGCAGCTCAGAT	815						
QY	541	CACAGCGCTGTGAGAGAGCTCCTACTGTAAGCGAAGACTTATTAACCAACCGGCTCT	600						
Db	816	CACAGCGCTGTGAGAGAGCTCCTACTGTAAGCGAAGACTTATTAACCAACCGGCTCT	875						
QY	601	CTCTCTCACACCTTATCCCGCCACCTGTGTGGGCTACCAATGCAATGAATG	660						

Db 876 CCTCTCCACACCACTCATTCCGCCCACTGTGTGGGGCTGACCAATGCAACTCAATG 935
OY 661 TCGTCAAAAGGAGAGACCACCTGCTCTCTCTTACTCTTATGCAATGTCCTCA 720
Db 936 TCGTCAAAAGGAGAGACCACCTGCTCTCTCTTACTCTTATGCAATGTCCTCA 995
OY 721 CATCTCTGGGGGAAAAATTTCTAGTATTTTGAATTTTGAATCTTACAGCAAAATAG 780
Db 996 CATCTCTGGGGGAAAAATTTCTAGTATTTTGAATTTTGAATCTTACAGCAAAATAG 1055
OY 781 GAACCTCTGGGGGAAAAATTTCTAGTATTTTGAATTTTGAATCTTACAGCAAAATAG 840
Db 1056 GAACCTCTGGGGGAAAAATTTCTAGTATTTTGAATTTTGAATCTTACAGCAAAATAG 1115
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Db 1116 CAACAAAAATGTGTGGCAATGAAATATATCAAGCAATATCTCCACCAAGGCTCT 1175
OY 901 GTAACTGGGACCAATGATTACTCTATAGGCTGTGTGAGATTTAGATGAATACCTG 960
Db 1176 GTAACTGGGACCAATGATTACTCTATAGGCTGTGTGAGATTTAGATGAATACCTG 1235
OY 961 TGAAGTGGCTAGGAGCTGCGCCAGCAATAGAGGCAATCAATGAACTTTTTCATAT 1020
Db 1236 TGAAGTGGCTAGGAGCTGCGCCAGCAATAGAGGCAATCAATGAACTTTTTCATAT 1295
OY 1021 AAA 1023
Db 1296 AAA 1298

RESULT 3
AK027683 1228 bp mRNA linear PRI 15-MAY-2001
LOCUS AK027683
DEFINITION Homo sapiens CDNA FLJ14777 fis. clone NT2RP4000259, weakly similar
to GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).
ACCESSION AK027683
VERSION AK027683.1 GI:14042545
KEYWORDS oligo cloning; fis (full insert sequence).
SOURCE Homo sapiens testicular carcinoma cell line:NT2 CDNA to mRNA,
clone:lib:NT2RP4 clone:NT2RP4000259.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Aotsuka,S., Yoshikawa,Y.,
Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Negahari,K., Masuho,Y. and Sasaki,N.
TITLE NEDD human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1228)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEDD human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
FEATURES
Source Location/Qualifiers
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/db_xref="taxon:9606"
/clone="NT2RP4000259"
/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP4"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal

precursor cells after 2-weeks retinoic acid (RA)
induction."
40..603
/note="unnamed protein product"
/protein_id="BAB5294.1"
/db_xref="GI:14042546"
/translation="MVAATVAAWLLLAACAOEODFYDFKAVINIRGLVLEKRY
GSLSLVVAVASEGFTDOHRALOLDJGPHHNVLAFCPNQGOEPPDSNKEIES
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BASE COUNT 326 a 330 c 290 g 282 t
ORIGIN

Query Match 85.7%; Score 919; DB 9; Length 1228;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 GAGCCGCCACCTCCGGAACAACCAATGTTGGGCGGAGGAGGAGCGGCGTGGCT 60
Db 15 GAGCCGCCACCTCCGGAACAACCAATGTTGGGCGGAGGAGGAGCGGCGTGGCT 74
OY 61 CCTGTGGGCTGGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db 75 CCTGTGGGCTGGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 134
OY 121 CATCCGGGCAAACTGTTGCTGCTGAGAGAAATACCCGGATGCTGCTGCTGCTGA 180
Db 135 CATCCGGGCAAACTGTTGCTGCTGAGAGAAATACCCGGATGCTGCTGCTGCTGA 194
OY 181 TGTGGCCAGCAGTGTGGGCTTGCAGACAGCAGCAGCAGCAGCAGCAGCAGCAGC 240
Db 195 TGTGGCCAGCAGTGTGGGCTTGCAGACAGCAGCAGCAGCAGCAGCAGCAGCAGC 254
OY 241 AGACCTGGGCGCCACACCTTCAACGTGCTGCTTCCCTCCCTGCAACCAAGTTGG 300
Db 255 AGACCTGGGCGCCACACCTTCAACGTGCTGCTTCCCTCCCTGCAACCAAGTTGG 314
OY 301 GAGGCGTGCAGCAGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
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OY 361 CCCCATGTTTGAACAATGTCATGTCACCGGATGCTGTCGCTTCCCTCAAGTACCT 420
Db 375 CCCCATGTTTGAACAATGTCATGTCACCGGATGCTGTCGCTTCCCTCAAGTACCT 434
OY 421 GGCCTCAGACTTCTGGAGAGAGCCACCTGGAACCTTGGAGTACCTTACGCCACAG 480
Db 435 GGCCTCAGACTTCTGGAGAGAGCCACCTGGAACCTTGGAGTACCTTACGCCACAG 494
OY 481 TGGAAAGGTGTGGGCGTGGGAGCCCACTGTGTCAGTGGAGAGAGTCAAGTCCAG 540
Db 495 TGGAAAGGTGTGGGCGTGGGAGCCCACTGTGTCAGTGGAGAGAGTCAAGTCCAG 554
OY 541 CACAGGCTCTGTGAGAGAGCTCATCTCTAGTGAAGAGAGAGAGAGAGAGAGAG 600
Db 555 CACAGGCTCTGTGAGAGAGCTCATCTCTAGTGAAGAGAGAGAGAGAGAGAGAG 614
OY 601 CCGTCTCAGCAGCTCATCTCCGCGCCACCTGTGTGGGCTGACCAATGCAAAATG 660
Db 615 CCGTCTCAGCAGCTCATCTCCGCGCCACCTGTGTGGGCTGACCAATGCAAAATG 674
OY 661 TCGTCAAAAGGAGAGACCACTGACCTGCTCTTACTCTTATGCAATGTCCTCA 720
Db 675 TCGTCAAAAGGAGAGACCACTGACCTGCTCTTACTCTTATGCAATGTCCTCA 734
OY 721 CATCTCTGGGGGAAAAATTTCTAGTATTTTGAATTTTGAATCTTACAGCAAAATAG 780
Db 735 CATCTCTGGGGGAAAAATTTCTAGTATTTTGAATTTTGAATCTTACAGCAAAATAG 794
OY 781 GAACCTCTGGGGGAAAAATTTCTAGTATTTTGAATTTTGAATCTTACAGCAAAATAG 840

Db 795 GAACCTCGGCCAATGAGAGCTCTTGACAGTGATACACCAGCCGATAGGAACCTCTTGC 854
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Db 855 CAACAAAAATGTGTGCAATATAGATATATCAAGCAATATCTCCACCAGGCTTC 914
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Db 915 GTAACTGGGACCAATGATTACCTCATAGGCTGTTGTGAGATTAGATGAATACCTG 974
QY 961 TGAATGCTGTAGGAGCTGCGACCCAAATAGAGGCAATCAATGATTTTTCATAT 1020
Db 975 TGAATGCTGTAGGAGCTGCGACCCAAATAGAGGCAATCAATGATTTTTCATAT 1034
QY 1021 AAACCAAAAAATGATTGTTATCAATAAAACTTGCATCCACATGAATTC 1072
Db 1035 AAACCAAAAAATGATTGTTATCAATAAAACTTGCATCCACATGAATTC 1086

RESULT 4
AX080813 1227 bp DNA linear PAT 27-FEB-2001
LOCUS Sequence 59 from Patent WO0109327.
DEFINITION AX080813
ACCESSION AX080813 GI:13169783
VERSION AX080813.1
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1227)
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,
Klajav, I.J., Lafleur, M., Mark, M.R., Masters, S.A., Pitt, R.M.,
Watanabe, C.K. and Wood, W.I.
TITLE Method of preventing the injury or death of retinal cells and
treating ocular diseases
JOURNAL Patent: WO 0109327-A 59 08-FEB-2001;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
source 1..1227
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 331 a 325 c 293 g 278 t
ORIGIN

Query Match 85.4%; Score 916; DB 6; Length 1227;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1066; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCGCCACCTCCGGAACAAGCCATGTTGGGCGGAGCGGTGGAGCGGCTGCTCTCT 63
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QY 64 GTGGGCTGGGCTGCGGCGAGAGAGAGAGACTTCTACGACTTCAAGCGGTCAACAT 123
Db 72 GTGGGCTGGGCTGCGGCGAGAGAGAGAGACTTCTACGACTTCAAGCGGTCAACAT 131
QY 124 CCGGGGCAAACTGTGTCGTGGAGAAGTACCGCGGATGCGTCCCTGGTGTGATGT 183
Db 132 CCGGGGCAAACTGTGTCGTGGAGAAGTACCGCGGATGCGTCCCTGGTGTGATGT 191
QY 184 GGCACAGAGTGGGCTTCACAGACGACACTACCGAGCCTTCACAGCTGCAGGAG 243
Db 192 GGCACAGAGTGGGCTTCACAGACGACACTACCGAGCCTTCACAGCTGCAGGAG 251
QY 244 CTTGGGCCCCCACCACCTTACGCTGCTGCTCCCTGCAACCAAGTTGGCCACAG 303
Db 252 CTTGGGCCCCCACCACCTTACGCTGCTGCTCCCTGCAACCAAGTTGGCCACAG 311
QY 304 GCGTACAGCAACAGAGATTGAGAGCTTTGCTGCGGACCTACAGTGTCAATTCC 363
Db 312 GCGTACAGCAACAGAGATTGAGAGCTTTGCTGCGGACCTACAGTGTCAATTCC 371

QY 364 CATGTTAGCAAGATTGCAATCCGGTACTGTGTCCTTCCATCTGCTTCAAGTACTGGC 423
Db 372 CATGTTAGCAAGATTGCAATCCGGTACTGTGTCCTTCCATCTGCTTCAAGTACTGGC 431
QY 424 CCAGACTTCTGGAGAGAGCCACCTGTGAACCTTGTGAAGTACTGATAGCCAGATGG 483
Db 432 CCAGACTTCTGGAGAGAGCCACCTGTGAACCTTGTGAAGTACTGATAGCCAGATGG 491
QY 484 AAGGTGTAGGGGCTTGGAGACCAGTGTGAGTGGAGGTGAGCTCCAGATCAG 543
Db 492 AAGGTGTAGGGGCTTGGAGACCAGTGTGAGTGGAGGTGAGCTCCAGATCAG 551
QY 544 AGCGCTGTGAGAGAGCCACCTGCTACTGAGAGAGAGAGATTATACCAACCGCTCTCT 603
Db 552 AGCGCTGTGAGAGAGCCACCTGCTACTGAGAGAGAGAGATTATACCAACCGCTCTCT 611
QY 604 CTTCCACACCTCATCTCCGCCACCTGTGTGGGCTGTGACCAATGCAAACTCAATGTGC 663
Db 612 CTTCCACACCTCATCTCCGCCACCTGTGTGGGCTGTGACCAATGCAAACTCAATGTGC 671
QY 664 TTCAAGGGAGAGAGCCACCTGCTCTCTTCTACTGATGCGATGTCATGTCAT 723
Db 672 TTCAAGGGAGAGAGCCACCTGCTCTCTTCTACTGATGCGATGTCATGTCAT 731
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QY 844 CAATAATGTGTGCAATATGAATATATCAAGCAATATCTCCACCAGGCTTCTGTA 903
Db 852 CAATAATGTGTGCAATATGAATATATCAAGCAATATCTCCACCAGGCTTCTGTA 911
QY 904 AACTGGAGCAATGATTACCTCATAGGCTGTTGTGAGATTAGATGAATACCTGTGA 963
Db 912 AACTGGAGCAATGATTACCTCATAGGCTGTTGTGAGATTAGATGAATACCTGTGA 971
QY 964 AAGTGGCTTAGGAGCTGCGACGCAAAATAGAGAGGATTCATGAACATTTTTCATATA 1023
Db 972 AAGTGGCTTAGGAGCTGCGACGCAAAATAGAGAGGATTCATGAACATTTTTCATATA 1031
QY 1024 CCAAAAAATGATTGTTATCAATAAAACTTGCATCCACATGAATTC 1072
Db 1032 CCAAAAAATGATTGTTATCAATAAAACTTGCATCCACATGAATTC 1080

RESULT 5
AF091092 857 bp mRNA linear PRI 12-NOV-1998
LOCUS Homo sapiens clone 683 unknown mRNA, complete sequence.
DEFINITION AF091092
ACCESSION AF091092
VERSION AF091092.1 GI:3860021
KEYWORDS FLI_CDNA.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 857)
AUTHORS Barrow, I.K.-P., Boguski, M.S., Touchman, J., and Spencer, F.
TITLE Full-insert sequence of mapped XREF EST
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 857)
AUTHORS Barrow, I.K.-P., Boguski, M.S., Touchman, J., and Spencer, F.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-1998) NHGRI, NIH, 49 Convent Drive, Building 49,
Room 2C08, Bethesda, MD 20892, USA
FEATURES
source 1..857
/organism="Homo sapiens"

/db_xref="taxon:9606"
/chromosome="1"
/map="1q24-q41"
/clone="683"
/note="location inferred using conservation of synteny
with mouse locus D1X1379"
46..225
/note="similar to Saccharomyces cerevisiae ORF YBR244W"
CDS
267 a 216 c 184 g 190 t
BASE COUNT
ORIGIN

Query Match 62.2%; Score 667; DB 9; Length 857;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 767; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

255 ACCACTTCACGTCGTCGCTTCCCTGACACAGTTGGCCACAGAGAGCTGACAGCA 314
|||||
10 ACCACTTCACGTCGTCGCTTCCCTGACACAGTTGGCCACAGAGAGCTGACAGCA 69
|||||
315 ACAAGAGATTGAGAGCTTGCCTGCGACCTACAGTGTCTCATTCCTCCATGTTAGCA 374
|||||
70 ACAAGAGATTGAGAGCTTGCCTGCGACCTACAGTGTCTCATTCCTCCATGTTAGCA 129
|||||
375 ACATTGCACTACACGGTACTGTGTCCTGCTTCAAGTACCTGGCCACAGCTTCTG 434
|||||
130 ACATTGCACTACACGGTACTGTGTCCTGCTTCAAGTACCTGGCCACAGCTTCTG 189
|||||
435 GGAAGAGCCACCTGGAGCTTCTGGAATGACTAGTACCTGACCTGGAAGAGAGTGA 494
|||||
190 GGAAGAGCCACCTGGAGCTTCTGGAATGACTAGTACCTGAGCCAGATGGAAGTGTAG 249
|||||
495 GGGCTTGGAGCCCACTGTGTGAGTGAAGAGTGTGAGTCCAGATCAGAGCTGCTGTA 554
|||||
250 GGGCTTGGAGCCCACTGTGTGAGTGAAGAGTGTGAGTCCAGATCAGAGCTGCTGTA 309
|||||
555 GGAAGTCACTCTACTGAAAGCAAGACTTATACCACTGGCTCTCTCTCCACCCACC 614
|||||
310 GGAAGTCACTCTACTGAAAGCAAGACTTATACCACTGGCTCTCTCTCCACCCACC 369
|||||
615 TCATCCCGCCACCTGTGTGAGGCTGACCAATGCAAACTGATGCTTCAAAAGGAG 674
|||||
370 TCATCCCGCCACCTGTGTGAGGCTGACCAATGCAAACTGATGCTTCAAAAGGAG 429
|||||
675 AGACCCACCTGCT 734
|||||
430 AGACCCACCTGCT 489
|||||
735 AAAAATTCAGTATTTTGTATTTTGAATCTTACAGCAAAATAGGAAGTCTCTGCCCA 794
|||||
490 AAAAATTCAGTATTTTGTATTTTGAATCTTACAGCAAAATAGGAAGTCTCTGCCCA 549
|||||
795 TGAGAGCTCTGTGACGATGATACACAGCGATAGGAAGTCTGTGCCAACAAAATGTGT 854
|||||
550 TGAGAGCTCTGTGACGATGATACACAGCGATAGGAAGTCTGTGCCAACAAAATGTGT 609
|||||
855 GGCAGATAGAGATATATCAAGCAATATCTCCACCAAGGCTTCTGTAAAGTGGAGCA 914
|||||
610 GGCAGATAGAGATATATCAAGCAATATCTCCACCAAGGCTTCTGTAAAGTGGAGCA 669
|||||
915 ATGATTAATCTCATAGGCTGTGTGTGAGATTAAGATGAATATCTGTAAAGTGGAGCA 974
|||||
670 ATGATTAATCTCATAGGCTGTGTGTGAGATTAAGATGAATATCTGTAAAGTGGAGCA 729
|||||
975 CAGTGCAGCAAAATAGAGGATTCATGAACATTTTGTGATATATATAA 1023
|||||
730 CAGTGCAGCAAAATAGAGGATTCATGAACATTTTGTGATATATATAA 778
|||||

RESULT 6
AX080809
LOCUS AX080809 1251 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 55 from Patent WO0109327.
ACCESSION AX080809
VERSION AX080809.1 GI:13169779
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..1251
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Partial DNA sequence used to isolate DNAs7037."
unsure
BASE COUNT 343 a 328 c 298 g 280 t 2 others
ORIGIN

Query Match 58.7%; Score 629; DB 6; Length 1251;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

395 GGTGCCATCTCTGCTTCAAGTACCTGCGCCAGACTTCTGGAGAGAGCCACCTGGAAC 454
|||||
401 GGTGCCATCTCTGCTTCAAGTACCTGCGCCAGACTTCTGGAGAGAGCCACCTGGAAC 460
|||||
455 TTCTGGAAGTACTAGTACGCCAGATGGAAGTGTGGGCTTGGAGCCACCTGTAAG 514
|||||
461 TTCTGGAAGTACTAGTACGCCAGATGGAAGTGTGGGCTTGGAGCCACCTGTAAG 520
|||||
515 TCAGTGGAGAGGTGAGTCCAGATCAGAGCTGCTGTGAGAGTCACTCTACTGTAAG 574
|||||
521 TCAGTGGAGAGGTGAGTCCAGATCAGAGCTGCTGTGAGAGTCACTCTACTGTAAG 580
|||||
575 CGAGAAGACTTATTAACACCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 634
|||||
581 CGAGAAGACTTATTAACACCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 640
|||||
635 GGGCTGACCAATGCAAACTGATGCTTCAAAAGGAGAGCCACAGTACCTCTCTCTCT 694
|||||
641 GGGCTGACCAATGCAAACTGATGCTTCAAAAGGAGAGCCACAGTACCTCTCTCTCT 700
|||||
695 CTCTACTTATGCACTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 754
|||||
701 CTCTACTTATGCACTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 760
|||||
755 TATTTGAATCTTACAGCAAAATAGGAAGTCTGTGCCAATGAGAGCTTGTGACAGTGA 814
|||||
761 TATTTGAATCTTACAGCAAAATAGGAAGTCTGTGCCAATGAGAGCTTGTGACAGTGA 820
|||||
815 ATACACAGCGATAGAGAGCTGTGCCAACAAAATGTGTGCAATATAGAAATATATCA 874
|||||
821 ATACACAGCGATAGAGAGCTGTGCCAACAAAATGTGTGCAATATAGAAATATATCA 880
|||||
875 GCAATATCTCCACCAAGGCTTCTGTAAAGTGGAGCAATGATTAATCTCATAGGAGCTG 934
|||||
881 GCAATATCTCCACCAAGGCTTCTGTAAAGTGGAGCAATGATTAATCTCATAGGAGCTG 940
|||||
935 TTGTGAGATTAAGAGAAATATCTGTGAAAGTGTGAGAGCTGCGACGCAAAATAGAG 994
|||||

Db 941 TTGTGAGATTAGGATGAATACCTGTGAAGTGCCTAGCAGCTGCCAGCCAAATAGAG 1000
QY 995 GCATTCATGACATTTTTCATATATA 1023
Db 1001 GCATTCATGACATTTTTCATATATA 1029

RESULT 7
AL356976 160066 bp DNA linear HTG 08-FEB-2002
LOCUS Homo sapiens chromosome 1 clone RP4-700P11 map p32.1-32.3, ***
DEFINITION SEQUENCING IN PROGRESS ***, 5 unordered pieces.
ACCESSION AL356976
VERSION AL356976.18 GI:18643752
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Van Hellmond, Z.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 10, 2002 this sequence version replaced gi:18477299.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
Project Information
Center project name: dj700P11
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 6% of reads
Dye-terminator Big Dye; 93% of reads
Consensus quality: 157881 bases at least Q40
Consensus quality: 158654 bases at least Q30
Consensus quality: 159095 bases at least Q20
Insert size: 159666; sum-of-contrigs
Insert size: 111224; 66.8% error; agarose-fp
Quality coverage: 7.58% in Q20 bases; sum-of-contrigs Quality
coverage: 12.72% in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 87143: contrig of 87143 bp in length
* 87144 87243: gap of 100 bp
* 87244 94440: contrig of 7197 bp in length
* 94441 94540: gap of 100 bp
* 94541 117956: contrig of 23416 bp in length
* 117957 118056: gap of 100 bp
* 118057 157663: contrig of 39607 bp in length
* 157664 157763: gap of 100 bp
* 157764 160066: contrig of 2303 bp in length.
Location/Qualifiers
1. 160066
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="p32.1-32.3"
/clone="RP4-700P11"
/clone_1db="RPI-4"
misc_feature
1..87143
/note="assembly_fragment:01501"

misc_feature
87244..94440
/note="assembly_fragment:00811
fragment_chain:1"
misc_feature
94541..117956
/note="assembly_fragment:02643
fragment_chain:1"
118057..157663
/note="assembly_fragment:03016
fragment_chain:1"
misc_feature
157764..160066
/note="assembly_fragment:01821"
BASE COUNT 42972 a 35602 c 36676 g 44415 t 401 others
ORIGIN

Query Match 55.6%; Score 596; DB 2; Length 160066;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 426 AGACTTCTGGGAAGAGAGCCACCTGACACTTGTGGAAGTACCTAGTACGAGATGAA 485
|||||
Db 112388 AGACTTCTGGGAAGAGAGCCACCTGACACTTGTGGAAGTACCTAGTACGAGATGAA 112329
QY 486 AGCTGTAGAGGCGCTTGGCAAGCCAACTGTGTCAAGTGGAGAGAGTCAAGTCCAGATCAG 545
|||||
Db 112328 AGCTGTAGAGGCGCTTGGCAAGCCAACTGTGTCAAGTGGAGAGAGTCAAGTCCAGATCAG 112269
QY 546 CGCTGTGAGAGAACTGATCTTACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
|||||
Db 112268 CGCTGTGAGAGAACTGATCTTACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 112209
QY 606 TCACACACCTCATCCGCCACCTGTGTGGGGGTGACCAATGCAAACTCAATGGTCTT 665
|||||
Db 112208 TCACACACCTCATCCGCCACCTGTGTGGGGGTGACCAATGCAAACTCAATGGTCTT 112149
QY 666 CAAAGGAG 725
|||||
Db 112148 CAAAGGAG 112089
QY 726 TTGTGGGGGAAAAATCTGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 785
|||||
Db 112088 TTGTGGGGGAAAAATCTGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 112029
QY 786 CTTGGCCAAATGAG 845
|||||
Db 112028 CTTGGCCAAATGAG 111969
QY 846 AAAATGTGTGGCAATATAGATATATCAAGCAATATATCCACCCAGAGAGAGAGAGAGAGAG 905
|||||
Db 111968 AAAATGTGTGGCAATATAGATATATCAAGCAATATATCCACCCAGAGAGAGAGAGAGAGAG 111909
QY 906 CTGGGACCAATGATTTACCTATAG 965
|||||
Db 111908 CTGGGACCAATGATTTACCTATAG 111849
QY 966 GTGCTTAG 1025
|||||
Db 111848 GTGCTTAG 111789
QY 1026 AAAAAATTAACCTGTTATCAATATATCAATATATCAATATATCAATATATCAATATATCAATATAT 1072
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Db 111788 AAAAAATTAACCTGTTATCAATATATCAATATATCAATATATCAATATATCAATATATCAATATAT 111742

RESULT 8
AX186595
LOCUS AX186595/C 751 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 2290 from Patent WO0142467.
ACCESSION AX186595
VERSION AX186595.1 GI:15138034
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 751)
 AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
 TITLE Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer
 JOURNAL Patent: WO 0142467-A 2290 14-JUN-2001;
 Millennium Predictive Medicine, Inc. (US)

FEATURES
 source location/Qualifiers
 1..751
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 194 a 141 c 143 g 269 t 4 others

ORIGIN

Query Match 33.7%; Score 361; DB 6; Length 751;
 Best Local Similarity 100.0%; Pred. No. 8.4e-204;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 712 TGTCCCATCATCTTGTGGGGGAAAAATTTAGTATTTTGAATTTGATCTTACAGC 771
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 DB 684 TGTCCCATCATCTTGTGGGGGAAAAATTTAGTATTTTGAATTTGATCTTACAGC 625
 |||||||
 QY 772 AACAAATAGGAAGTCTGGGCAATGAGAGCTCTTGACAGATGATCCAGCGATACGA 831
 |||||||
 DB 624 AACAAATAGGAAGTCTGGGCAATGAGAGCTCTTGACAGATGATCCAGCGATACGA 565
 |||||||
 QY 832 AGCTCTGGCAACAAAATGTGTGGCAATAGATATATCAAGCAATATCTCCACCC 891
 |||||||
 DB 564 AGCTCTGGCAACAAAATGTGTGGCAATAGATATATCAAGCAATATCTCCACCC 505
 |||||||
 QY 892 AAGGCTTCTGTAAGTGGGAGCAATGATATACCTCATAGGAGCTTGTGGAGATTAGATG 951
 |||||||
 DB 504 AAGGCTTCTGTAAGTGGGAGCAATGATATACCTCATAGGAGCTTGTGGAGATTAGATG 445
 |||||||
 QY 952 AATATACCTGTGAAAGTGCCTAGGAGCTGCGCAAGCAATAGAGGAGCATTCATGACATTT 1011
 |||||||
 DB 444 AATATACCTGTGAAAGTGCCTAGGAGCTGCGCAAGCAATAGAGGAGCATTCATGACATTT 385
 |||||||
 QY 1012 TTTGCATATTAACCAAAAATTAATCTGTATCAATAAAACTTGATCCACATGATTT 1071
 |||||||
 DB 384 TTTGCATATTAACCAAAAATTAATCTGTATCAATAAAACTTGATCCACATGATTT 325
 |||||||
 QY 1072 C 1072
 |
 DB 324 C 324

RESULT 9
 AX187668/c 468 bp DNA linear PAT 06-AUG-2001
 LOCUS AX187668
 DEFINITION Sequence 3363 from Patent WO0142467.
 ACCESSION AX187668
 VERSION AX187668.1 GI:15139132
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 468)
 AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
 TITLE Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer
 JOURNAL Patent: WO 0142467-A 3363 14-JUN-2001;
 Millennium Predictive Medicine, Inc. (US)

FEATURES
 source location/Qualifiers
 1..468
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 131 a 84 c 94 g 159 t

ORIGIN

Query Match 33.2%; Score 356; DB 6; Length 468;
 Best Local Similarity 100.0%; Pred. No. 7.9e-201;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 CCATCATCTTGTGGGGGAAAAATTTAGTATTTTGAATTTGATCTTACAGCAACAA 776
 |||||||
 DB 468 CCATCATCTTGTGGGGGAAAAATTTAGTATTTTGAATTTGATCTTACAGCAACAA 409
 |||||||
 QY 777 ATAGGAACCTCTGGGCAATGAGAGCTCTTGACAGATGATCCAGCGATACGAACCTC 836
 |||||||
 DB 408 ATAGGAACCTCTGGGCAATGAGAGCTCTTGACAGATGATCCAGCGATACGAACCTC 349
 |||||||
 QY 837 TTGCCAACAATAATGTGTGGCAATGAGATATATCAAGCAATATCTCCACCCAGGC 896
 |||||||
 DB 348 TTGCCAACAATAATGTGTGGCAATGAGATATATCAAGCAATATCTCCACCCAGGC 289
 |||||||
 QY 897 TTCTGTAAGTGGGACCAATGATATACCTCATAGGAGCTTGTGGAGATTAGATGAATA 956
 |||||||
 DB 288 TTCTGTAAGTGGGACCAATGATATACCTCATAGGAGCTTGTGGAGATTAGATGAATA 229
 |||||||
 QY 957 CCTGTAAAGTGCCTTAGGAGAGTCCAGCAATAGAGGAGCATTCATGAACTTTTGC 1016
 |||||||
 DB 228 CCTGTAAAGTGCCTTAGGAGAGTCCAGCAATAGAGGAGCATTCATGAACTTTTGC 169
 |||||||
 QY 1017 ATATAACCAAAAATTAATCTGTATCAATAAAACTTGATCCACATGATTTTC 1072
 |||||||
 DB 168 ATATAACCAAAAATTAATCTGTATCAATAAAACTTGATCCACATGATTTTC 113
 |||||||

RESULT 10
 AF322456 51381 bp DNA linear HTG 06-DEC-2000
 LOCUS AF322456
 DEFINITION Homo sapiens chromosome 17 clone BAC629B10 map 17p13.3, ***
 SEQUENCING IN PROGRESS ***, 120 unordered pieces.
 ACCESSION AF322456
 VERSION AF322456.1 GI:11559861
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 51381)
 AUTHORS Zhao, X.T., He, M., Wan, D.F., Ye, Y., Qin, W.X., Huang, Y., Zuo, L. and Gu, J.R.
 TITLE Gene clone on human chromosome 17p13.3
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 51381)
 AUTHORS Zhao, X.T., He, M., Wan, D.F., Ye, Y., Qin, W.X., Huang, Y., Zuo, L. and Gu, J.R.
 TITLE Direct Submission
 JOURNAL Submitted (21-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Jun 2200 Xie-Tu Road, Shanghai 200032, P. R. China

COMMENT
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 120 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 236: contig of 236 bp in length
 * 237 435: contig of 199 bp in length
 * 436 665: contig of 230 bp in length
 * 666 879: contig of 214 bp in length
 * 880 1121: contig of 242 bp in length
 * gap of unknown length
 * gap of unknown length

*	1122	1948: contig of 827 bp in length	*	16827	gap of unknown length
*		gap of unknown length	*		17628: contig of 802 bp in length
*	1949	2628: contig of 680 bp in length	*		gap of unknown length
*		gap of unknown length	*	17629	contig of 695 bp in length
*	2629	3229: contig of 601 bp in length	*		18323: contig of 695 bp in length
*		gap of unknown length	*	18324	gap of unknown length
*	3230	3893: contig of 664 bp in length	*		18532: contig of 209 bp in length
*		gap of unknown length	*	18533	gap of unknown length
*	3894	4090: contig of 197 bp in length	*		18742: contig of 210 bp in length
*		gap of unknown length	*	18743	gap of unknown length
*	4091	4272: contig of 182 bp in length	*		19453: contig of 711 bp in length
*		gap of unknown length	*	19454	gap of unknown length
*	4273	4420: contig of 148 bp in length	*		20109: contig of 656 bp in length
*		gap of unknown length	*	20110	gap of unknown length
*	4421	4633: contig of 213 bp in length	*		20724: contig of 615 bp in length
*		gap of unknown length	*	20725	gap of unknown length
*	4634	5219: contig of 586 bp in length	*		21417: contig of 693 bp in length
*		gap of unknown length	*	21418	gap of unknown length
*	5220	5881: contig of 662 bp in length	*		21679: contig of 262 bp in length
*		gap of unknown length	*	21680	gap of unknown length
*	5882	6118: contig of 237 bp in length	*		21888: contig of 209 bp in length
*		gap of unknown length	*	21889	gap of unknown length
*	6119	6334: contig of 216 bp in length	*		22072: contig of 184 bp in length
*		gap of unknown length	*	22073	gap of unknown length
*	6335	6484: contig of 150 bp in length	*		22788: contig of 716 bp in length
*		gap of unknown length	*	22789	gap of unknown length
*	6485	6623: contig of 139 bp in length	*		23448: contig of 660 bp in length
*		gap of unknown length	*	23449	gap of unknown length
*	6624	6861: contig of 238 bp in length	*		23658: contig of 210 bp in length
*		gap of unknown length	*	23659	gap of unknown length
*	6862	7067: contig of 206 bp in length	*		23869: contig of 211 bp in length
*		gap of unknown length	*	23870	gap of unknown length
*	7068	7836: contig of 769 bp in length	*		24449: contig of 580 bp in length
*		gap of unknown length	*	24450	gap of unknown length
*	7837	8541: contig of 705 bp in length	*		25107: contig of 658 bp in length
*		gap of unknown length	*	25108	gap of unknown length
*	8542	8731: contig of 190 bp in length	*		25316: contig of 209 bp in length
*		gap of unknown length	*	25317	gap of unknown length
*	8732	8875: contig of 144 bp in length	*		25526: contig of 210 bp in length
*		gap of unknown length	*	25527	gap of unknown length
*	8876	9094: contig of 219 bp in length	*		25902: contig of 376 bp in length
*		gap of unknown length	*	25903	gap of unknown length
*	9095	9684: contig of 590 bp in length	*		26555: contig of 653 bp in length
*		gap of unknown length	*	26556	gap of unknown length
*	9685	10350: contig of 666 bp in length	*		26764: contig of 209 bp in length
*		gap of unknown length	*	26765	gap of unknown length
*	10351	10528: contig of 178 bp in length	*		26973: contig of 209 bp in length
*		gap of unknown length	*	26974	gap of unknown length
*	10529	11128: contig of 600 bp in length	*		27587: contig of 614 bp in length
*		gap of unknown length	*	27588	gap of unknown length
*	11129	11784: contig of 656 bp in length	*		27796: contig of 209 bp in length
*		gap of unknown length	*	27797	gap of unknown length
*	11785	11991: contig of 207 bp in length	*		27997: contig of 201 bp in length
*		gap of unknown length	*	27998	gap of unknown length
*	11992	12648: contig of 657 bp in length	*		28229: contig of 232 bp in length
*		gap of unknown length	*	28230	gap of unknown length
*	12649	13323: contig of 675 bp in length	*		28451: contig of 222 bp in length
*		gap of unknown length	*	28452	gap of unknown length
*	13324	13607: contig of 284 bp in length	*		29087: contig of 636 bp in length
*		gap of unknown length	*	29088	gap of unknown length
*	13608	13833: contig of 226 bp in length	*		29741: contig of 654 bp in length
*		gap of unknown length	*	29742	gap of unknown length
*	13834	14452: contig of 619 bp in length	*		29980: contig of 239 bp in length
*		gap of unknown length	*	29981	gap of unknown length
*	14453	15107: contig of 655 bp in length	*		30204: contig of 224 bp in length
*		gap of unknown length	*	30205	gap of unknown length
*	15108	15743: contig of 636 bp in length	*		30725: contig of 521 bp in length
*		gap of unknown length	*	30726	gap of unknown length
*	15744	16395: contig of 652 bp in length	*		31377: contig of 652 bp in length
*		gap of unknown length	*	31378	gap of unknown length
*	16396	16614: contig of 219 bp in length	*		31587: contig of 210 bp in length
*		gap of unknown length	*	31588	gap of unknown length
*	16615	16826: contig of 212 bp in length	*		31792: contig of 205 bp in length
*		gap of unknown length	*		gap of unknown length

Query Match
Best Local Similarity 14.1% Score 151; DB 2: Length 51381;
Matches 201: Conservative 0; Pred. No. 5.2e-78; Mismatches 1; Indels 0; Gaps 0;

QY 136 GGTGTCGTGAGAACTACCGGATCGATCGTCCCTGCTGATGATGCGCAGCAGTGTG 195
|||||
Db 50834 GGTGTCGTGAGAACTACCGGATCGATCGTCCCTGCTGATGATGCGCAGCAGTGTG 50893

QY 196 CGGCTTCACAGACACAGACTACGAGCCCTGCGACAGCTGCGACGAGACCTGGCCCCCA 255
|||||
Db 50894 CGGCTTCACAGACACAGACTACGAGCCCTGCGACAGCTGCGACGAGACCTGGCCCCCA 50953

QY 256 CCACCTCAACGTCGTCGCTCCCTGCAACGATTTGGCCACAGAGCCTGACAGCAA 315
|||||
Db 50954 CCACCTCAACGTCGTCGCTCCCTGCAACGATTTGGCCACAGAGCCTGACAGCAA 51013

QY 316 CAAGGAGATTGAGAGCTTTGCC 337
|||||
Db 51014 CAAGGAGATTGAGAGCTTTGCC 51035

RESULT 11
AF322456 51381 bp DNA linear HTG 06-DEC-2000
LOCUS AF322456/c
DEFINITION Homo sapiens chromosome 17 clone BAC629B10 map 17p13.3. ***
ACCESSION AF322456
VERSION AF322456.1 GI:11559861
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 51381)
Zhao,X.T., He,M., Wan,D.F., Ye,Y., Qin,W.X., Huang,Y., Zuo,L. and
Gu,J.R.
Gene clone on human chromosome 17p13.3
Unpublished
2 (bases 1 to 51381)
Zhao,X.T., He,M., Wan,D.F., Ye,Y., Qin,W.X., Huang,Y., Zuo,L. and
Gu,J.R.
Direct Submission
Submitted (21-NOV-2000) National Laboratory For Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/ln 2200 Xie-Tu Road, Shanghai
200032, P. R. China
* NOTE: This is a 'working draft' sequence. It currently
* consists of 120 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 236: contig of 236 bp in length
* gap of unknown length
* 237 435: contig of 199 bp in length
* gap of unknown length
* 436 665: contig of 230 bp in length

666 gap of unknown length
879: contig of 214 bp in length
gap of unknown length
880 1121: contig of 242 bp in length
gap of unknown length
1122 1948: contig of 827 bp in length
gap of unknown length
1949 2628: contig of 680 bp in length
gap of unknown length
2629 3229: contig of 601 bp in length
gap of unknown length
3230 3893: contig of 664 bp in length
gap of unknown length
3894 4090: contig of 197 bp in length
gap of unknown length
4091 4272: contig of 182 bp in length
gap of unknown length
4273 4420: contig of 148 bp in length
gap of unknown length
4421 4633: contig of 213 bp in length
gap of unknown length
4634 5219: contig of 586 bp in length
gap of unknown length
5220 5881: contig of 662 bp in length
gap of unknown length
5882 6118: contig of 237 bp in length
gap of unknown length
6119 6334: contig of 216 bp in length
gap of unknown length
6335 6484: contig of 150 bp in length
gap of unknown length
6485 6623: contig of 139 bp in length
gap of unknown length
6624 6861: contig of 238 bp in length
gap of unknown length
6862 7067: contig of 206 bp in length
gap of unknown length
7068 7836: contig of 769 bp in length
gap of unknown length
7837 8541: contig of 705 bp in length
gap of unknown length
8542 8731: contig of 190 bp in length
gap of unknown length
8732 8875: contig of 144 bp in length
gap of unknown length
8876 9094: contig of 219 bp in length
gap of unknown length
9095 9684: contig of 590 bp in length
gap of unknown length
9685 10350: contig of 666 bp in length
gap of unknown length
10351 10528: contig of 178 bp in length
gap of unknown length
10529 11128: contig of 600 bp in length
gap of unknown length
11129 11784: contig of 656 bp in length
gap of unknown length
11785 11991: contig of 207 bp in length
gap of unknown length
11992 12648: contig of 657 bp in length
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12649 13323: contig of 675 bp in length
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13324 13607: contig of 284 bp in length
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13608 13833: contig of 226 bp in length
gap of unknown length
13834 14452: contig of 619 bp in length
gap of unknown length
14453 15107: contig of 655 bp in length
gap of unknown length
15108 15743: contig of 636 bp in length
gap of unknown length

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* 15744 16395: contig of 652 bp in length
* 16396 16614: contig of 219 bp in length
* 16615 16826: contig of 212 bp in length
* 16827 17628: contig of 802 bp in length
* 17629 18323: contig of 695 bp in length
* 18324 18532: contig of 209 bp in length
* 18533 18742: contig of 210 bp in length
* 18743 19453: contig of 711 bp in length
* 19454 20109: contig of 656 bp in length
* 20110 20724: contig of 615 bp in length
* 20725 21417: contig of 693 bp in length
* 21418 21679: contig of 262 bp in length
* 21680 21888: contig of 209 bp in length
* 21889 22072: contig of 184 bp in length
* 22073 22788: contig of 716 bp in length
* 22789 23448: contig of 660 bp in length
* 23449 23658: contig of 210 bp in length
* 23659 23869: contig of 211 bp in length
* 23870 24449: contig of 580 bp in length
* 24450 25107: contig of 658 bp in length
* 25108 25316: contig of 209 bp in length
* 25317 25526: contig of 210 bp in length
* 25527 25902: contig of 376 bp in length
* 25903 26555: contig of 653 bp in length
* 26556 26764: contig of 209 bp in length
* 26765 26973: contig of 209 bp in length
* 26974 27587: contig of 614 bp in length
* 27588 27796: contig of 209 bp in length
* 27797 27997: contig of 201 bp in length
* 27998 28229: contig of 232 bp in length
* 28230 28451: contig of 222 bp in length
* 28452 29087: contig of 636 bp in length
* 29088 29741: contig of 654 bp in length
* 29742 29980: contig of 239 bp in length
* 29981 30204: contig of 224 bp in length
* 30205 30725: contig of 521 bp in length
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* 31378 31587: contig of 210 bp in length
* 31588 31792: contig of 205 bp in length
* 31793 32403: contig of 611 bp in length
* 32404 33056: contig of 653 bp in length
* 33057 33266: contig of 210 bp in length
* 33267 33471: contig of 205 bp in length
* 33472 34137: contig of 666 bp in length
* 34138 34789: contig of 652 bp in length
* 34790 35003: contig of 214 bp in length
* gap of unknown length

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-35;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 846 AAAATGTGGCAATAGATATCAAGCAATATCTCCACCCAGGCTTGTAA 905
DB 49797 AAAATGTGGCAATAGATATCAAGCAATATCTCCACCCAGGCTTGTAA 49738
QY 906 CTGGGACCAATGATTCCTC 925
DB 49737 CTGGGACCAATGATTCCTC 49718

RESULT 12
AC022847 55891 bp DNA linear HTG 06-FEB-2000
LOCUS Homo sapiens chromosome 11 clone RP11-261F7 map 11, LOW-PASS
DEFINITION
SEQUENCE SAMPLING.
ACCESSION AC022847
VERSION AC022847.1 GI:6922212
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 55891)
REFERENCE Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-261F7
2 (bases 1 to 55891)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Becker, R., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dearellano, K., Dewar, K., Domingo, M., Doyle, M., Feneator, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Garayna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lander, T., Lechoczek, J., Levine, R., Liu, C., Liu, G., Locke, K.,
Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheters, R., Meldrum, J., Menais, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/xk/RepeatMasker.html

```

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6164
Center clone name: 261_F_7

* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1	698:	contig of 698 bp in length
699	1436:	gap of unknown length
1437	2155:	gap of unknown length
2156	2866:	contig of 719 bp in length
2867	3559:	gap of unknown length
3560	4266:	gap of 693 bp in length
4267	4955:	contig of 707 bp in length
4956	5656:	gap of unknown length
5657	6372:	contig of 701 bp in length
6373	7082:	gap of unknown length
7083	7807:	contig of 716 bp in length
7808	8527:	gap of unknown length
8528	9248:	contig of 720 bp in length
9249	9953:	gap of unknown length
9954	10663:	contig of 721 bp in length
10664	11392:	gap of 705 bp in length
11393	12092:	contig of 710 bp in length
12093	12805:	gap of unknown length
12806	13523:	contig of 713 bp in length
13524	14261:	gap of unknown length
14262	14967:	gap of 718 bp in length
14968	15698:	contig of 731 bp in length
15699	16427:	gap of unknown length
16428	17145:	contig of 729 bp in length
17146	17851:	gap of unknown length
17852	18565:	contig of 716 bp in length
18566	19394:	gap of unknown length

[illegible]

SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (sites)
JOURNAL Direct Submission
Submitted (30-Oct-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Nov 1, 2001 this sequence version replaced gi:16508350.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BM46M23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 23827 bases at least Q40
Consensus quality: 239150 bases at least Q30
Insert size: 239848; sum-of-contigs
Insert size: 228542; 2.6% error; agarose-fp
Quality coverage: 8.48x in Q20 bases; sum-of-contigs Quality
coverage: 10.79x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
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Location/Qualifiers
1..241048
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
/clone_1fb="RP23-46M23"
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/note="assembly_fragment:05780"
4461..50623
/note="assembly_fragment:03143"
fragment_chain:1"
50724..55265
/note="assembly_fragment:04670"
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/note="assembly_fragment:01496"
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100580..139135
/note="assembly_fragment:01557"
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139236..158187
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/note="assembly_fragment:04424"
fragment_chain:1"
181846..191755
/note="assembly_fragment:00436"
fragment_chain:1"
191856..196544
/note="assembly_fragment:04437"
fragment_chain:1"
196645..238408

/note="assembly_fragment:06204"
fragment_chain:1"
238509..241048
/note="assembly_fragment:02545"
fragment_chain:1"
clone_end:SP6
vector_side:right"
BASE COUNT 66632 a 51150 c 52737 g 69313 t 1216 others
ORIGIN

Query Match 4.3%; Score 46; DB 2; Length 241048;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 426 AGACTTCTGGAGAGAGCCACCTGGAAGTCTGGAAGTACCTAGT 471
|||||
Db 132611 AGACTTCTGGAGAGAGCCACCTGGAAGTCTGGAAGTACCTAGT 132566

Search completed: August 25, 2002, 07:16:27
Job time: 5781 sec

